SEQUENCE LISTING

<110> Stern, David M.
      Schmidt, Ann Marie
      Yan, Shi Du
      Zlokovic, Berislav

<120> A METHOD TO INCREASE CEREBRAL BLOOD FLOW IN AMYLOID
      ANGIOPATHY

<130> 0575/62097

<140> Not Yet Known
<141> 2000-08-14

<160> 6

<170> PatentIn Ver. 2.1

<210> 1
<211> 416
<212> PRT
<213> Bos Taurus

<400> 1
Met Ala Ala Gly Ala Val Val Gly Ala Trp Met Leu Val Leu Ser Leu
 1   5   10   15

Gly Gly Thr Val Thr Gly Asp Gln Asn Ile Thr Ala Arg Ile Gly Lys
            20   25   30

Pro Leu Val Leu Asn Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
            35   40   45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
    50   55   60

Ser Pro Gln Gly Asp Pro Trp Asp Ser Val Ala Arg Val Leu Pro Asn
 65   70   75   80

Gly Ser Leu Leu Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Thr Phe
                85   90   95

Arg Cys Arg Ala Thr Ser Arg Ser Gly Lys Glu Thr Lys Ser Asn Tyr
                100   105   110

Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
                115   120   125

1

```
Ala Ser Glu Leu Met Ala Gly Val Pro Asn Lys Val Gly Thr Cys Val
    130                 135                 140

Ser Glu Gly Gly Tyr Pro Ala Gly Thr Leu Asn Trp Leu Leu Asp Gly
145                 150                 155                 160

Lys Thr Leu Ile Pro Asp Gly Lys Gly Val Ser Val Lys Glu Glu Thr
                165                 170                 175

Lys Arg His Pro Lys Thr Gly Leu Phe Thr Leu His Ser Glu Leu Met
                180                 185                 190

Val Thr Pro Ala Arg Gly Gly Ala Leu His Pro Thr Phe Ser Cys Ser
                195                 200                 205

Phe Thr Pro Gly Leu Pro Arg Arg Arg Ala Leu His Thr Ala Pro Ile
    210                 215                 220

Gln Leu Arg Val Trp Ser Glu His Arg Gly Gly Glu Gly Pro Asn Val
225                 230                 235                 240

Asp Ala Val Pro Leu Lys Glu Val Gln Leu Val Val Glu Pro Glu Gly
                245                 250                 255

Gly Ala Val Ala Pro Gly Gly Thr Val Thr Leu Thr Cys Glu Ala Pro
                260                 265                 270

Ala Gln Pro Pro Pro Gln Ile His Trp Ile Lys Asp Gly Arg Pro Leu
    275                 280                 285

Pro Leu Pro Pro Gly Pro Met Leu Leu Leu Pro Glu Val Gly Pro Glu
    290                 295                 300

Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr His Pro Ser His Gly Pro
305                 310                 315                 320

Gln Glu Ser Arg Ala Val Ser Val Thr Ile Ile Glu Thr Gly Glu Glu
                325                 330                 335

Gly Thr Thr Ala Gly Ser Val Glu Gly Pro Gly Leu Glu Thr Leu Ala
                340                 345                 350

Leu Thr Leu Gly Ile Leu Gly Gly Leu Gly Thr Val Ala Leu Leu Ile
    355                 360                 365

Gly Val Ile Val Trp His Arg Arg Arg Gln Arg Lys Gly Gln Glu Arg
    370                 375                 380
```

2

Lys Val Pro Glu Asn Gln Glu Glu Glu Glu Glu Arg Ala Glu Leu
385   390   395   400

Asn Gln Pro Glu Glu Pro Glu Ala Ala Glu Ser Ser Thr Gly Gly Pro
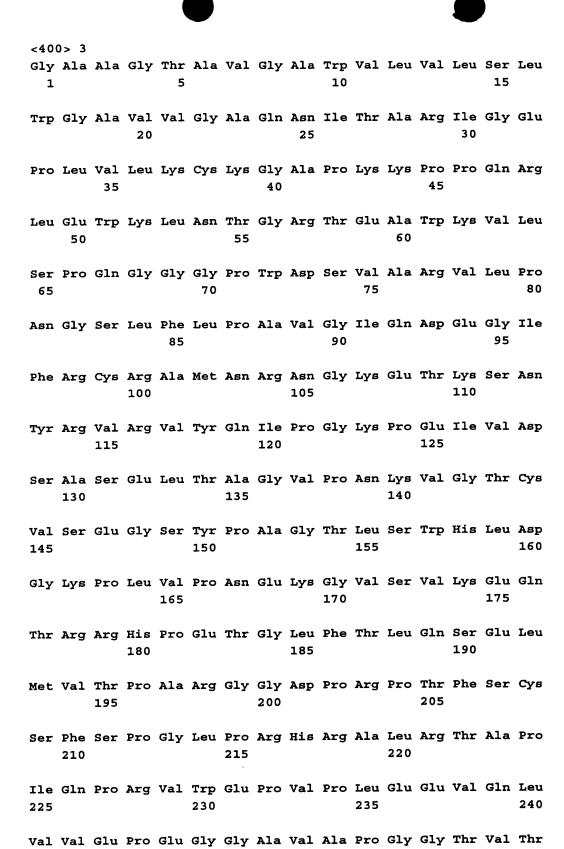   405   410   415

<210> 2
<211> 1426
<212> DNA
<213> Bos Taurus

<400> 2
cggagaagga tggcagcagg ggcagtggtc ggagcctgga tgctagtcct cagtctgggg 60
gggacagtca cggggggacca aaacatcaca gcccggatcg ggaagccact ggtgctgaac 120
tgcaagggag ccccccaagaa accaccccag cagctggaat ggaaactgaa cacaggccgg 180
acagaagctt ggaaagtcct gtctccccag ggagacccct gggatagcgt ggctcgggtc 240
ctccccaacg gctccctcct cctgccggct gttgggatcc aggatgaggg gactttccgg 300
tgccgggcaa cgagccggag cggaaaggag accaagtcta actaccgagt ccgagtctat 360
cagattcctg ggaagccaga aattgttgat cctgcctctg aactcatggc tggtgtcccc 420
aataaggtgg ggacatgtgt gtccgagggg ggctaccctg cagggactct taactggctc 480
ttggatggga aaactctgat tcctgatggc aaaggagtgt cagtgaagga agagaccaag 540
agacacccaa agacagggct tttcacgctc cattcggagc tgatggtgac cccagctcgg 600
ggaggagctc tccaccccac cttctcctgt agcttcaccc ctggccttcc ccggcgccga 660
gccctgcaca cggccccccat ccagctcagg gtctggagtg agcaccgagg tggggagggc 720
cccaacgtgg acgctgtgcc actgaaggaa gtccagttgg tggtagagcc agaaggggga 780
gcagtagctc ctggtggtac tgtgaccttg acctgtgaag ccccccgccca gcccccacct 840
caaatccact ggatcaagga tggcaggccc ctgcccccttc ccctggccc catgctgctc 900
ctcccagagg tagggcctga ggaccaggga acctacagtt gtgtggccac ccatcccagc 960
catgggcccc aggagagccg tgctgtcagc gtcacgatca tcgaaacagg cgaggagggg 1020
acgactgcag gctctgtgga agggccgggg ctggaaaccc tagccctgac cctggggatc 1080
ctgggaggcc tggggacagt cgccctgctc attggggtca tcgtgtggca tcgaaggcgg 1140
caacgcaaag gacaggagag gaaggtcccg gaaaaccagg aggaggaaga ggaggagaga 1200
gcggaactga accagccaga ggagcccgag gcggcagaga gcagcacagg agggcccttga 1260
ggagcccacg gccagacccg atccatcagc ccctttctt ttcccacact ctgttctggc 1320
cccagaccag ttctcctctg tataatctcc agcccacatc tcccaaactt tcttccacaa 1380
ccagagcctc ccacaaaaag tgatgagtaa acacctgcca cattta 1426

<210> 3
<211> 404
<212> PRT
<213> Human

3

<400> 3

Gly Ala Ala Gly Thr Ala Val Gly Ala Trp Val Leu Val Leu Ser Leu
 1   5   10   15

Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
            20   25   30

Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
            35   40   45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
        50   55   60

Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
65   70   75   80

Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
                85   90   95

Phe Arg Cys Arg Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn
            100   105   110

Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp
            115   120   125

Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys
    130   135   140

Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp
145   150   155   160

Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
            165   170   175

Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu
            180   185   190

Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys
            195   200   205

Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro
    210   215   220

Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu
225   230   235   240

Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr
            245   250   255

4

Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met
        260   265   270

Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu
        275   280   285

Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr
        290   295   300

His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
305   310   315   320

Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
                325   330   335

Gly Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly
                340   345   350

Thr Ala Ala Leu Leu Ile Gly Val Ile Leu Trp Gln Arg Arg Gln Arg
        355   360   365

Arg Gly Glu Glu Arg Lys Ala Pro Glu Asn Gln Glu Glu Glu Glu Glu
        370   375   380

Arg Ala Glu Leu Asn Gln Ser Glu Glu Pro Glu Ala Gly Glu Ser Ser
385   390   395   400

Thr Gly Gly Pro
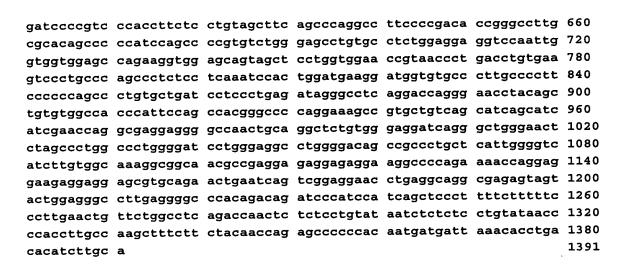

<210> 4
<211> 1391
<212> DNA
<213> Human

<400> 4
ggggcagccg gaacagcagt tggagcctgg gtgctggtcc tcagtctgtg gggggcagta 60
gtaggtgctc aaaacatcac agcccggatt ggcgagccac tggtgctgaa gtgtaagggg 120
gcccccaaga aaccacccca gcggctggaa tggaaactga acacaggccg gacagaagct 180
tggaaggtcc tgtctcccca gggaggaggc ccctgggaca gtgtggctcg tgtccttccc 240
aacggctccc tcttccttcc ggctgtcggg atccaggatg aggggatttt ccggtgcagg 300
gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt 360
cctgggaagc cagaaattgt agattctgcc tctgaactca cggctggtgt tcccaataag 420
gtggggacat gtgtgtcaga gggaagctac cctgcaggga ctcttagctg gcacttggat 480
gggaagcccc tggtgcctaa tgagaaggga gtatctgtga aggaacagac caggagacac 540
cctgagacag ggctcttcac actgcagtcg gagctaatgg tgaccccagc ccggggagga 600

5

```
gatccccgtc ccaccttctc ctgtagcttc agcccaggcc ttccccgaca ccgggccttg 660
cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg 720
gtggtggagc cagaaggtgg agcagtagct cctggtggaa ccgtaaccct gacctgtgaa 780
gtccctgccc agccctctcc tcaaatccac tggatgaagg atggtgtgcc cttgcccctt 840
ccccccagcc ctgtgctgat cctccctgag atagggcctc aggaccaggg aacctacagc 900
tgtgtggcca cccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc 960
atcgaaccag gcgaggaggg gccaactgca ggctctgtgg gaggatcagg gctgggaact 1020
ctagccctgg ccctggggat cctgggaggc ctggggacag ccgccctgct cattggggtc 1080
atcttgtggc aaaggcggca acgccgagga gaggagagga aggccccaga aaaccaggag 1140
gaagaggagg agcgtgcaga actgaatcag tcggaggaac ctgaggcagg cgagagtagt 1200
actggagggc cttgaggggc ccacagacag atcccatcca tcagctccct tttcttttttc 1260
ccttgaactg ttctggcctc agaccaactc tctcctgtat aatctctctc ctgtataacc 1320
ccaccttgcc aagctttctt ctacaaccag agcccccac aatgatgatt aaacacctga 1380
cacatcttgc a                                                    1391
```

<210> 5
<211> 403
<212> PRT
<213> Mouse

<400> 5

```
Met Pro Ala Gly Thr Ala Ala Arg Ala Trp Val Leu Val Leu Ala Leu
 1               5                  10                  15

Trp Gly Ala Val Ala Gly Gly Gln Asn Ile Thr Ala Arg Ile Gly Glu
              20                  25                  30

Pro Leu Val Leu Ser Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln
          35                  40                  45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
      50                  55                  60

Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Gln Ile Leu Pro Asn
65                  70                  75                  80

Gly Ser Leu Leu Leu Pro Ala Thr Gly Ile Val Asp Glu Gly Thr Phe
                  85                  90                  95

Arg Cys Arg Ala Thr Asn Arg Arg Gly Lys Glu Val Lys Ser Asn Tyr
              100                 105                 110

Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro
          115                 120                 125

Ala Ser Glu Leu Thr Ala Ser Val Pro Asn Lys Val Gly Thr Cys Val
          130                 135                 140
```
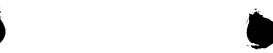
6

```
Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp Gly
145             150             155             160

Lys Leu Leu Ile Pro Asp Gly Lys Glu Thr Leu Val Lys Glu Glu Thr
                165             170             175

Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Arg Ser Glu Leu Thr
                180             185             190

Val Ile Pro Thr Gln Gly Gly Thr Thr His Pro Thr Phe Ser Cys Ser
                195             200             205

Phe Ser Leu Gly Leu Pro Arg Arg Arg Pro Leu Asn Thr Ala Pro Ile
        210             215             220

Gln Leu Arg Val Arg Glu Pro Gly Pro Pro Glu Gly Ile Gln Leu Leu
225             230             235             240

Val Glu Pro Glu Gly Gly Ile Val Ala Pro Gly Gly Thr Val Thr Leu
                245             250             255

Thr Cys Ala Ile Ser Ala Gln Pro Pro Pro Gln Val His Trp Ile Lys
                260             265             270

Asp Gly Ala Pro Leu Pro Leu Ala Pro Ser Pro Val Leu Leu Leu Pro
                275             280             285

Glu Val Gly His Ala Asp Glu Gly Thr Tyr Ser Cys Val Ala Thr His
        290             295             300

Pro Ser His Gly Pro Gln Glu Ser Pro Pro Val Ser Ile Arg Val Thr
305             310             315             320

Glu Thr Gly Asp Glu Gly Pro Ala Glu Gly Ser Val Gly Glu Ser Gly
                325             330             335

Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly Val
                340             345             350

Val Ala Leu Leu Val Gly Ala Ile Leu Trp Arg Lys Arg Gln Pro Arg
        355             360             365

Arg Glu Glu Arg Lys Ala Pro Glu Ser Gln Glu Asp Glu Glu Glu Arg
        370             375             380

Ala Glu Leu Asn Gln Ser Glu Glu Ala Glu Met Pro Glu Asn Gly Ala
385             390             395             400
```

7

Gly Gly Pro

<210> 6
<211> 1347
<212> DNA
<213> Mouse

<400> 6
gcaccatgcc agcgggggaca gcagctagag cctgggtgct ggttcttgct ctatggggag 60
ctgtagctgg tggtcagaac atcacagccc ggattggaga gccacttgtg ctaagctgta 120
aggggccccc taagaagccg ccccagcagc tagaatggaa actgaacaca ggaagaactg 180
aagcttggaa ggtcctctct ccccagggag gccctggga cagcgtggct caaatcctcc 240
ccaatggttc cctcctcctt ccagccactg gaattgtcga tgaggggacg ttccggtgtc 300
gggcaactaa caggcgaggg aaggaggtca agtccaacta ccgagtccga gtctaccaga 360
ttcctgggaa gccagaaatt gtggatcctg cctctgaact cacagccagt gtccctaata 420
aggtggggac atgtgtgtct gagggaagct accctgcagg gacccttagc tggcacttag 480
atgggaaact tctgattccc gatggcaaag aaacactcgt gaaggaagag accaggagac 540
accctgagac gggactcttt acactgcggt cagagctgac agtgatcccc acccaaggag 600
gaaccaccca tcctaccttc tcctgcagtt tcagcctggg ccttcccgg cgcagacccc 660
tgaacacagc ccctatccaa ctccgagtca gggagcctgg gcctccagag ggcattcagc 720
tgttggttga gcctgaaggt ggaatagtcg ctcctggtgg gactgtgacc ttgacctgtg 780
ccatctctgc ccagcccct cctcaggtcc actggataaa ggatggtgca cccttgcccc 840
tggctcccag ccctgtgctg ctcctccctg aggtggggca cgcggatgag ggcacctata 900
gctgcgtggc cacccaccct agccacggac ctcaggaaag ccctcctgtc agcatcaggg 960
tcacagaaac cggcgatgag gggccagctg aaggctctgt gggtgagtct gggctgggta 1020
cgctagccct ggccttgggg atcctgggag gcctgggagt agtagccctg ctcgtcgggg 1080
ctatcctgtg gcgaaaacga caacccaggc gtgaggagag gaaggccccg gaaagccagg 1140
aggatgagga ggaacgtgca gagctgaatc agtcagagga agcggagatg ccagagaatg 1200
gtgccggggg accgtaagag cacccagatc gagcctgtgt gatggcccta gagcagctcc 1260
cccacattcc atcccaattc ctccttgagg cacttccttc tccaaccaga gcccacatga 1320
ccatgctgag taaacatttg atacggc 1347